

# SEQUENCE PROTOCOL

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<130> 000493 BT

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10 <141>

<160> 4

<170> PatentIn Ver. 2.1

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<213> Corynebacterium glutamicum

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ccactaaaca gcttcaatca attcgggtgc cactccaaca tgtaga gtg gtg cgc 235

Met Val Arg

1

35

gtt aaa aaa gtt ttc cta att ttc att ttc tta aaa gga gct cgc cag 283

Val Lys Lys Val Phe Leu Ile Phe Ile Phe Leu Lys Gly Ala Arg Gln

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40

gac atg gca cag gtt atg gac ttc aag gtt gcc gat ctt tca cta gca 331

Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala

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gag gca gga cgt cac cag att cgt ctt gca gag tat gag atg cca ggt 379

Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly

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ctc atg cag ttg cgc aag gaa ttc gca gac gag cag cct ttg aag ggc 427

Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly

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gcc cga att gct ggt tct atc cac atg acg gtc cag acc gcc gtg ctt 475

Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu

70

75

80

att gag acc ctc act gct ttg ggc gct gag gtt cgt tgg gct tcc tgc 523

Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys

85

90

95

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aac att ttc tcc acc cag gat gag gct gca gcg gct atc gtt gtc ggc 571

Asn 100 ile Phe Ser Thr Gln 105 Asp Glu Ala Ala 110 Ala Ile Val Val Gly 115  
 5 tcc ggc acc gtc gaa gag cca gct ggt gtt cca gta ttc gcg tgg aag 619  
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 10 ggt gag tca ctg gag gag tac tgg tgg tgc atc aac cag atc ttc agc 667  
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 15 tgg ggc gat gag ctg cca aac atg atc ctc gac gac ggc ggt gac gcc 715  
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 20 cca cca gca gag gcc aac gat tcc gat gag tac atc gca ttc ttg ggc 811  
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 30 gct gag gcc gtt aag ggt gtc acc gag gaa acc acc acc ggt gtg cac 907  
 Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His  
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 35 cgc ctg tac cac ttc gct gaa gaa ggc gtg ctg cct ttc cca gcg atg 955  
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 230 235 240  
 40 aac gtc aac gac gct gtc acc aag tcc aag ttt gat aac aag tac ggc 1003  
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 Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu  
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 55 gaa gct gac cca atc aac gct ctt cag gct ctg atg gat ggc tac tct 1195  
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 310 315 320

See  
 al  
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gtg gtc acc gtt gat gag gcc atc gag gac gcc gac atc gtg atc acc 1243  
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325 330 335

5 gcg acc ggc aac aag gac atc att tcc ttc gag cag atg ctc aag atg 1291  
Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met  
340 345 350 355

10 aag gat cac gct ctg ctg ggc aac atc ggt cac ttt gat aat gag atc 1339  
Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile  
360 365 370

15 gat atg cat tcc ctg ttg cac cgc gac gac gtc acc cgc acc acg atc 1387  
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375 380 385

aag cca cag gtc gac gag ttc acc ttc tcc acc ggt cgc tcc atc atc 1435  
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20 gtc ctg tcc gaa ggt cgc ctg ttg aac ctt ggc aac gcc acc gga cac 1483  
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25 cca tca ttt gtc atg tcc aac tct ttc gcc gat cag acc att gcg cag 1531  
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30 atc gaa ctg ttc caa aac gaa gga cag tac gag aac gag gtc tac cgt 1579  
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35 ctg cct aag gtt ctc gac gaa aag gtg gca cgc atc cac gtt gag gct 1627  
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40 ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag gct gag tac atc 1675  
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45 ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac tac cgc tac 1720  
Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr  
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50 taatgattgt cagcattgag ggaatcgacg gcgcgggcaa aaacaccctg gtttcggcat 1780  
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at  
end

Ala Arg Gln Asp Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu  
20 25 30

5 Ser Leu Ala Glu Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu  
35 40 45

Met Pro Gly Leu Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro  
50 55 60

10 Leu Lys Gly Ala Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr  
65 70 75 80

Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp  
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15 Ala Ser Cys Asn Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile  
100 105 110

20 Val Val Gly Ser Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe  
115 120 125

Ala Trp Lys Gly Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln  
130 135 140

25 Ile Phe Ser Trp Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly  
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Gly Asp Ala Thr Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala  
165 170 175

30 Gly Leu Val Pro Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala  
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35 Phe Leu Gly Met Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp  
195 200 205

Gly Lys Ile Ala Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr  
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40 Gly Val His Arg Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe  
225 230 235 240

45 Pro Ala Met Asn Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn  
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Lys Tyr Gly Thr Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr  
260 265 270

50 Asp Met Leu Met Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp  
275 280 285

Val Gly Lys Gly Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val  
290 295 300

55 Lys Val Thr Glu Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp  
305 310 315 320

60 Gly Tyr Ser Val Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile  
325 330 335

Val Ile Thr Ala Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met  
 340 345 350  
 5 Leu Lys Met Lys Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp  
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 Asn Glu Ile Asp Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg  
 370 375 380  
 10 Thr Thr Ile Lys Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg  
 385 390 395 400  
 Ser Ile Ile Val Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala  
 405 410 415  
 15 Thr Gly His Pro Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr  
 420 425 430  
 20 Ile Ala Gln Ile Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu  
 435 440 445  
 Val Tyr Arg Leu Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His  
 450 455 460  
 25 Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala  
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